



## SEQUENCE LISTING

<110> Salkoff, Lawrence  
Schreiber, Matthew  
Silvia, Chris  
The Washington University  
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

B5  
BD  
<210> 1  
<211> 1112  
<212> PRT  
<213> Mus musculus

<220>  
<223> mouse Slo3 (mSlo3)

<220>  
<221> VARIANT  
<222> (5)  
<223> polymorphic variant #2 Leu -> Ile

<220>  
<221> VARIANT  
<222> (21)  
<223> polymorphic variant #1 Ile -> Val

<220>  
<221> VARIANT  
<222> (25)  
<223> polymorphic variant #3 Ala -> Ser

<400> 1  
Met Ser Gln Thr Leu Leu Asp Ser Leu Asn Gln Lys Glu Leu Thr Glu  
1 5 10 15  
Thr Ser Cys Thr Ile Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Leu  
20 25 30  
Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala  
35 40 45  
Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu  
50 55 60

Leu Glu Leu Phe Ser Ser Arg Arg Ile Glu Ala Asn Pro Leu Arg Lys  
65 70 75 80

Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser  
85 90 95

Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu  
100 105 110

Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val  
115 120 125

Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser  
130 135 140

Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala  
145 150 155 160

Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile  
165 170 175

Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp  
180 185 190

Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys  
195 200 205

Ile Leu Gln Ile Leu Gln Val Ile Lys Thr Ser Asn Ser Val Lys Leu  
210 215 220

Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly  
225 230 235 240

Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg  
245 250 255

Asn Ser Gln Thr Met Ser Tyr Phe Glu Ser Ile Tyr Leu Val Thr Ala  
260 265 270

Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu  
275 280 285

Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe  
290 295 300

Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys  
305 310 315 320

Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val  
325 330 335

Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe  
340 345 350

Leu His Trp Lys Ser Gly Glu Ile Asn Ile Glu Ile Val Phe Leu Gly  
355 360 365

Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr  
370 375 380

Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu  
 385 390 395 400  
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn  
 405 410 415  
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg  
 420 425 430  
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln  
 435 440 445  
 Ile Leu Gln Ser Gln Asn Lys Val Phe Leu Ser Lys Ile Pro Asn Trp  
 450 455 460  
 Asp Trp Ser Ala Gly Asp Asn Ile Leu Cys Phe Ala Glu Leu Lys Leu  
 465 470 475 480  
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu  
 485 490 495  
 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro  
 500 505 510  
 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln  
 515 520 525  
 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg  
 530 535 540  
 Leu Cys Phe Val Lys Leu Asn Leu Met Leu Ile Ala Ile Gln His Lys  
 545 550 555 560  
 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln  
 565 570 575  
 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser  
 580 585 590  
 Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp  
 595 600 605  
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser  
 610 615 620  
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu  
 625 630 635 640  
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu  
 645 650 655  
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr  
 660 665 670  
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu  
 675 680 685  
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys  
 690 695 700

Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His  
 705 710 715 720  
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu  
 725 730 735  
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu  
 740 745 750  
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu  
 755 760 765  
 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser  
 770 775 780  
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser  
 785 790 795 800  
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile  
 805 810 815  
 Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu  
 820 825 830  
 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro  
 835 840 845  
 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile  
 850 855 860  
 Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu  
 865 870 875 880  
 Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu  
 885 890 895  
 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp  
 900 905 910  
 Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu  
 915 920 925  
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu  
 930 935 940  
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys  
 945 950 955 960  
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr  
 965 970 975  
 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys  
 980 985 990  
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met  
 995 1000 1005  
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr  
 1010 1015 1020

Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys  
1025 1030 1035 1040

Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe  
1045 1050 1055

Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg His Trp Pro  
1060 1065 1070

Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile  
1075 1080 1085

Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr  
1090 1095 1100

Pro Glu Ser Ile Leu Trp Thr Arg  
1105 1110

<210> 2  
<211> 3339  
<212> DNA  
<213> Mus musculus

<220>  
<223> mouse Slo3 (mSlo3)

<400> 2  
atgtctcaaa cattgctaga cagtttaat cagaaggagt tgacggaaac gtcatgtaca 60  
atcgaaatcc aggcacgcgtt cattcttcc tccttggcga ctttcttcgg gggactcatc 120  
atcttattcc ttttcagaat agccttggaaa agctcaagaa gttggaaata cgtcaagggg 180  
ccaagaggac tcttggaaact attctcatca cgtagaatcg aggctaattcc ttggaggaaa 240  
ctttactttc atggagtatt tcgtcagcgc atcgaaatgc tgctttctgc acagaccgtc 300  
gtggggcaag tgggggtgat ctttgcgttt gtactaagca tcgggtctct tgtgatctat 360  
ttcatcaatt caatggatcc ttgtcgaagg ttgtcttcat atgaagacaa aattgtccat 420  
ggggatttga gtttcaacgc tttcttttagc ttctattttgggttggaggtt ttggggcagct 480  
gaagacaaga tcaagtctg gttggagatg aattcaattt tagacatttt taccatcccc 540  
ccaaaccttta tttcttattt tttgaagagt aattggctag gtttgagatt tctaagagct 600  
ctgcgggtgc tcgaactccc taaaatctt cagatcctac aagtcatcaa gaccagcaat 660  
tcagtgaagg tttccaaact gttgtcaata gttatcagta cctgggtcac ggcagcagga 720  
ttccttcacc tggggaaaa ttctgggtac ccctggctca acggaagaaa ctcacagact 780  
atgtcatact ttgagtctat ttatctgtg acagcaacaa tgtcaactgt tggctttggg 840  
gacgtgggtgg ccaagacatc cctaggacgg atttcattt gtttcttcat ccttggggagt 900  
ttgatactat ttgcaaaactt cattccagaa atgggtggac tcttttctac caggaagaaa 960  
tacaccaagc cttacgaagc agtcaaagga aaaaagttca tcgtggctcg tggaaacatc 1020  
acagttgaca gtgttactgc tttcttgagg aattttctcc actggaaatgc cggggaaatc 1080  
aatattgaga tcgttatttctt tggagagact ctcccttgct tggaaactggc gaccttactg 1140  
aagtgccaca catcctgtac caacttcgtt tgccggcaccc cactgaagtt cgaggatctg 1200  
aagcgagttt cagttggagaa ctccggagccg tgcctgattc tagccaaacca tttctgttagt 1260  
gacttacatg acgaagacaa ctcaaaccatt atgagggtgc tctcgatcaa gaactattat 1320  
ccacagacca gactcatcat tcagataactt cagttcaaa acaagtttt cctgtcaaaa 1380  
atcccccaact gggactggag tgcggagac aatattctt cttttgcaga gctaaagctc 1440  
ggatttatcg cccaaaggctg cttgggtgcca gggctgtgca cttttctcac gactctgttc 1500  
attgaacaaa accaaaaggt ttttcttaaa catccctggc aaaaacattt cttgaatggc 1560  
ttgaagaaca agattctgac acagcgctc tctaaccgact tcgtggggat gacatttccc 1620  
caggctctccc ggctctgtt tgcggacta aatctcatgc tgatcgccat ccaacacaag 1680  
cccttcttcc acagggtgtt cactctgata ctaaacccat catcccaagt gaggctgaat 1740  
aaggacaccc tgggttctt cattggggac tcctccaaag ccgtccaaag ggctttctt 1800  
tactgttcca actgtcacag cgtatgtgtc aatcctgagc taattggaaa gtgttaactgt 1860  
aaaatcaaga gccgacaaca actcatagca ccgaccatca tggtgatgaa aagcagctg 1920  
accgatttca ccacttcttc acacatccac gtttctatgt caacagaaat tcacacttgt 1980

tttcaagag aacaggctag tttgatcacc attacaacca acagaccaac gacaaacgac 2040  
 acagtggatg ataccgacat gctggacagc agtggcatgt ttcactggcg cagagcaatg 2100  
 cccttgaca aggtgttct gaaacgaagt gagaaggcaa aacacgagt tcagaaccac 2160  
 attgttagtat gcgtgttgg agatgccaa tgtaccctgg tggggcttcg gaatttcgtg 2220  
 atgcccctga gagccagcaa ctacacccgg caggagctga aggacattgt tttattggg 2280  
 tctctggagt acttccagag agaatggcgaa ttctccgaa actttcccaa gatacacatt 2340  
 atgcctggat ctgcactcta catggagat ctgattgcag tcaatgtaga gcagtgcct 2400  
 atgtgcgtca tcttagccac accctacaag gcactgagca gccagattct ggtggacaca 2460  
 gaggccatca tggccaccct caacatccag tccctgcgga tcaccagtcc tactccaggg 2520  
 tcttcaaagt cagaagtaaa gccatcatct gccttgata gtaaagaaag gaagcaaaga 2580  
 tacaacaga tccccattct cactgaactg aagaatccct ccaacatcca ctttatttgag 2640  
 cagatggcg gactggatgg aatgctaaa gggactagct tgcatctcag cacttcttc 2700  
 tccaccggtg ctgtctttc agacacccctc ttggattctc tcctggccac gtccttctac 2760  
 aattaccatg tcgtgaaatt acttcagatg cttagtactg gaggcataag ctctgagatg 2820  
 gaacactatt tggtaagga gaagccctat aagacaactg acgactatga ggcaatcaag 2880  
 tctgggagga cgccgtgtaa gctgggactc ctctctttag accaaaccgt tctatcaggc 2940  
 attaatccaa gaaaaacctt tggacagctg ttctgtggct cattggataa ttccgggatc 3000  
 ctatgtgtcg gcttataccg tatgattgtt gaagaggaac ccagccaaaga acacaaaagg 3060  
 tttgtatca ccaggccatc caatgagatgc cacctgctgc cctcagatct cgtttttgt 3120  
 gccatccctt tcaacaccac ctgtggcaaa tcagacagca gtccttcaa ttcaggcgc 3180  
 aaaacaactc tacaaacgcg acgacgccat tggcccgagg gtcgaatttc ttgcattcgc 3240  
 accatgccga cgagtccac gatcttacc cagtcgacga cacggagag aggtggtctc 3300  
 agcaccacca ctcccgagtc tatccttgg acacgttag 3339

<210> 3  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human Slo3-a (hSlo3-a)

<220>  
 <221> MOD\_RES  
 <222> (29)  
 <223> Xaa = any amino acid

<400> 3  
 Gly Leu Ala Ala Leu Ile Leu Ser Ser Phe Val Thr Leu Phe Ser Gly  
 1 5 10 15

Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys  
 20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser  
 35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln  
 50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly  
 65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile  
 85 90 95

Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile  
 100 105 110

<210> 4  
<211> 416  
<212> DNA  
<213> Homo sapiens

<220>  
<223> human Slo3 (hSlo3)

<400> 4  
ggcttgcag cgctcattct ttcctccttt gtgaccctct tcagtggact catcagcctg 60  
ttgatcttca ggctgtatctg gagayctgtt aaaaaatggc aaatcatcaa gggAACAGGA 120  
attatcttgg aactgttcac atcaggtaacc atcgcttagga gccatgtaaag aagcctccac 180  
ttccaggac aatttcgtga tcatatagaa atgttgctt cagcccagac ctttgtggg 240  
caagtgttgg tgatccttgc ctttgtacta agcattgggt ctcttataat ctatTCATC 300  
aattcwgctg accctgttgg aacgctgttc atcatatgaa gacaaaacca ttcctattga 360  
tttggttttc aatgcttctt tttagttctt ttttgggttg aggttttggc aaagcc 416

<210> 5  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo3 peptide starting with amino acid 687

<400> 5  
Met Leu Asp Ser  
1

<210> 6  
<211> 112  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human Slo3-b (hSlo3-b)

<220>  
<221> MOD\_RES  
<222> (29)  
<223> Xaa = any amino acid

<400> 6  
Gly Leu Ala Ala Leu Ile Leu Ser Ser Phe Val Thr Leu Phe Thr Gly  
1 5 10 15

Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys  
20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser  
35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln  
50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly  
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile  
85 90 95

Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile  
100 105 110

<210> 7  
<211> 112  
<212> PRT  
<213> Homo sapiens

<220>  
<223> human Slo3-c (hSLO3-c)

<220>  
<221> MOD\_RES  
<222> (29)  
<223> Xaa = any amino acid

<400> 7  
Gly Leu Ala Ala Leu Ile Leu Ser Ser Phe Val Thr Leu Phe Ser Gly  
1 5 10 15

Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys  
20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser  
35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln  
50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly  
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile  
85 90 95

Ile Tyr Phe Ile Asn Ser Met Asp Pro Val Gly Thr Leu Phe Ile Ile  
100 105 110

<210> 8  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 8  
ctcgaactcc ctaaaaatctt acagat

26

<210> 9  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 9  
ttccgtttag ccaggggtca ccagaatt

28

<210> 10  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 10  
tctgctttgt gaagctaaat ct

22

<210> 11  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 11  
tttcaaagcc tcttttagcgg taa

23

<210> 12  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 12  
ttatgcctgg atctgcactc tacatg

26

<210> 13  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSlo3 primer

<400> 13  
atagtttccg tctactaccg aaa

23

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:hSlo3 primer  
  
 <400> 14  
 ggcaagcgctc atttttttcc cctt 24

<210> 15  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:hSlo3 primer  
  
 <400> 15  
 tgccccaaac ctcaacccaa aata 24

<210> 16  
 <211> 1105  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human Slo3-1 (hSlo3-1)

<220>  
 <221> VARIANT  
 <222> (6)  
 <223> polymorphic variant #2 Leu -> Ile

<220>  
 <221> VARIANT  
 <222> (23)  
 <223> polymorphic variant #1 Ile -> Val

<220>  
 <221> VARIANT  
 <222> (25)  
 <223> polymorphic variant #3 Ala -> Ser

<400> 16  
 Met Phe Gln Thr Lys Leu Arg Asn Glu Thr Trp Glu Asp Leu Pro Lys  
                       5                         10                         15  
 1

Met Ser Cys Thr Thr Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Phe  
                       20                         25                         30

Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Ile Phe Arg Leu Ile  
                       35                         40                         45

Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile  
                       50                         55                         60

Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser  
                       65                         70                         75                         80

Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser  
                       85                         90                         95

Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu  
 100 105 110  
 Ser Ile Gly Ser Leu Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val  
 115 120 125  
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val  
 130 135 140  
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala  
 145 150 155 160  
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile  
 165 170 175  
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp  
 180 185 190  
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln  
 195 200 205  
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe  
 210 215 220  
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly  
 225 230 235 240  
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg  
 245 250 255  
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala  
 260 265 270  
 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu  
 275 280 285  
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe  
 290 295 300  
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ala Asn Lys Arg Lys  
 305 310 315 320  
 Tyr Thr Ser Ser Tyr Glu Ala Leu Lys Gly Lys Lys Phe Ile Val Val  
 325 330 335  
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe  
 340 345 350  
 Leu Arg Asp Lys Ser Gly Glu Ile Asn Thr Glu Ile Val Phe Leu Gly  
 355 360 365  
 Glu Thr Pro Pro Ser Leu Glu Leu Glu Thr Ile Phe Lys Cys Tyr Leu  
 370 375 380  
 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu  
 385 390 395 400  
 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn  
 405 410 415

Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg  
 420 425 430  
 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln  
 435 440 445  
 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp  
 450 455 460  
 Asn Trp Asp Thr Gly Asp Asn Ile Ile Cys Phe Ala Glu Leu Lys Leu  
 465 470 475 480  
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu  
 485 490 495  
 Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr  
 500 505 510  
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gln  
 515 520 525  
 Arg Leu Ser Asp Asp Phe Ala Gly Met Ser Phe Pro Glu Val Ala Arg  
 530 535 540  
 Leu Cys Phe Leu Lys Met Tyr Leu Leu Leu Ile Ala Ile Glu Tyr Lys  
 545 550 555 560  
 Ser Leu Phe Thr Asp Gly Phe Cys Gly Leu Ile Leu Asn Pro Pro Pro  
 565 570 575  
 Gln Val Arg Ile Arg Lys Asn Thr Leu Gly Phe Phe Ile Ala Glu Thr  
 580 585 590  
 Pro Lys Asp Val Arg Arg Ala Leu Phe Tyr Cys Ser Val Cys His Asp  
 595 600 605  
 Asp Val Phe Ile Pro Glu Leu Ile Thr Asn Cys Gly Cys Lys Ser Arg  
 610 615 620  
 Ser Arg Gln His Ile Thr Val Pro Ser Val Lys Arg Met Lys Lys Cys  
 625 630 635 640  
 Leu Lys Gly Ile Ser Ser Arg Ile Ser Gly Gln Asp Ser Pro Pro Arg  
 645 650 655  
 Val Ser Ala Ser Thr Ser Ser Ile Ser Asn Phe Thr Thr Arg Thr Leu  
 660 665 670  
 Gln His Asp Val Glu Gln Asp Ser Asp Gln Leu Asp Ser Ser Gly Met  
 675 680 685  
 Phe His Trp Cys Lys Pro Thr Ser Leu Asp Lys Val Thr Leu Lys Arg  
 690 695 700  
 Thr Gly Lys Ser Lys Tyr Lys Phe Arg Asn His Ile Val Ala Cys Val  
 705 710 715 720  
 Phe Gly Asp Ala His Ser Ala Pro Met Gly Leu Arg Asn Phe Val Met  
 725 730 735

Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val  
 740 745 750  
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg  
 755 760 765  
 Asn Phe Pro Gln Ile Tyr Ile Leu Pro Gly Cys Ala Leu Tyr Ser Gly  
 770 775 780  
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu  
 785 790 795 800  
 Ser Pro Pro Pro Gln Pro Ser Ser Asn Gln Thr Leu Val Asp Thr Glu  
 805 810 815  
 Ala Ile Met Ala Thr Leu Thr Ile Gly Ser Leu Gln Ile Asp Ser Ser  
 820 825 830  
 Ser Asp Pro Ser Pro Ser Val Ser Glu Glu Thr Pro Gly Tyr Thr Asn  
 835 840 845  
 Gly His Asn Glu Lys Ser Asn Cys Arg Lys Val Pro Ile Leu Thr Glu  
 850 855 860  
 Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu Gln Leu Gly Gly Leu  
 865 870 875 880  
 Glu Gly Ser Leu Gln Glu Thr Asn Leu His Leu Ser Thr Ala Phe Ser  
 885 890 895  
 Thr Gly Thr Val Phe Ser Ser Ser Phe Leu Asp Ser Leu Leu Ala Thr  
 900 905 910  
 Ala Phe Tyr Asn Tyr His Val Leu Glu Leu Leu Gln Met Leu Val Thr  
 915 920 925  
 Gly Gly Val Ser Ser Gln Leu Glu Gln His Leu Asp Lys Asp Lys Val  
 930 935 940  
 Tyr Gly Val Ala Asp Ser Cys Thr Ser Leu Leu Ser Gly Arg Asn Arg  
 945 950 955 960  
 Cys Lys Leu Gly Leu Leu Ser Leu His Glu Thr Ile Leu Ser Asp Val  
 965 970 975  
 Asn Pro Arg Asn Thr Phe Gly Gln Leu Phe Cys Gly Ser Leu Asp Leu  
 980 985 990  
 Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Ile Ile Asp Glu Glu Glu  
 995 1000 1005  
 Leu Asn Pro Glu Asn Lys Arg Phe Val Ile Thr Arg Pro Ala Asn Glu  
 1010 1015 1020  
 Phe Lys Leu Leu Pro Ser Asp Leu Val Phe Cys Ala Ile Pro Phe Ser  
 1025 1030 1035 1040  
 Thr Ala Cys Tyr Lys Arg Asn Glu Glu Phe Ser Leu Gln Lys Ser Tyr  
 1045 1050 1055

Glu Ile Val Asn Lys Ala Ser Gln Thr Thr Glu Asp Thr Phe Arg His  
1060 1065 1070

Lys Leu Ser Ser His Pro Leu Ile Gln Leu Leu Arg His Cys Ile His  
1075 1080 1085

Gln Ser Ile Leu Thr Ser Arg Glu Leu Thr Pro Ser Leu Phe Leu Ser  
1090 1095 1100

Lys  
1105

<210> 17  
<211> 3319  
<212> DNA  
<213> Homo sapiens

<220>  
<223> human Slo3-1 (hSlo3-1)

<400> 17  
atgtttcaga ctaagctacg aaatgaaact tgggaagact tgccaaaaat gtcctgcaca 60  
actgagatcc aagcagcatt cattctctt tcctttgtga ccttcttcag tggactcatc 120  
atcttgttga tcttcaggct gatctggaga tctgttaaaa aatggcaaata catcaaggga 180  
acaggaatta tcttggaaact gttcacatca ggtaccatcg ctaggagcca tctaagaagc 240  
ctccacttcc agggacaatt tcgtgatcat atagaaatgt tgcttcagc ccagaccttt 300  
gtggggcaag tgggggtgat ctttgtctt gtactaagca ttgggtctct tataatctat 360  
ttcatcaatt ctgctgaccc tggggaaacg tggcatcat atgaagacaa aaccattcc 420  
attgatttgg tttcaatgc tttcttttagt ttcttatttg gattgagggt tatggcagct 480  
gatgacaaga tcaagttctg gctggagatg aattcaatcg tagacatctt taccatccca 540  
ccaaccttta tttcttata tttggaaagc aattggctag gtttaagggtt cctaagagcc 600  
ttggccctgc tagaactccc tcaaatacttgc caaattctac gagccatcaa gaccagtaac 660  
tcagtgaagt tttccaaact gctgtcaata attctcgtt cctgggtcac agctgcggga 720  
ttcatttcacc tgggtggaaaa ttctgggtgat ccctggctca aaggtagaaa ttccacagaat 780  
atatcatatt ttgagtcattt ttagctggc atggcaacaa cgtcaaccgt tggatttgg 840  
gatgtggtag ccaagacatc ctttaggacgg accttcatca tggatcttcc actggggagt 900  
ttgatattat ttgcgaaact tatactgaa atgggtggaaac tggatcttcc caagaggaaa 960  
tacaccagt cmtatgaagc actcaaagga aagaagtttta ttgtggctg tggaaacatc 1020  
actgtggaca gtgtgaccgc tttcctgagg aatttcctcc ggcacaagtc aggagagatc 1080  
aacactgaaa ttgttttccctt ggggagaaacc cctccttctt tggaaacttga aaccatattt 1140  
aaatgctact tggccatcac aacgttcatt tctggatctg .caatgaagtgggatctg 1200  
aggcgagttt cgggtggaaatc tgcagaggca tgcctgatta tagccaatcc tttgtgcagt 1260  
gattcccatg ctgaagatatttccaaatcat atgagggtgc tctctatcaa gaactatgat 1320  
tctaccacca gaatcatcat acagatactg caatccata acaaggtttta tctgccaagg 1380  
atccccagctt ggaactggga caccggagac aacatcatct gctttgtga attaaaactt 1440  
ggatttatcg cccaggctg tttgggtgcca ggcttggatc ctttccatcc atctctatcc 1500  
gtggagcaaa acaaaaaggat tatgcctaaa cagaccttggaa agaaacactt cttgaatagc 1560  
ataaaaaaca aaattctgac ccaacgttcc tctgtatgtt ttgctggat gagctttcc 1620  
gaagttgccctt ggctctgtt tctgaagatg tacccctgt tgatagccat cgaatacaag 1680  
tcccttttta cggatggttt ctgtggatctg atactaaatc cacctccaca agtggggata 1740  
cgttggatcg ctttattgtt gaaactccaa aggacgttgc aagagccttgc 1800  
ttttactgtt cagttgtca tgatgtatgtt ttcatttcgtt agctaattac aaactgtggc 1860  
tgcaaaaagca gaaggccggca gcacatcaca gtgcctatcg taaagagaat gaaaaaaatgt 1920  
ctgaaggggaa tctcctctcg tatatcaggg caggatttcc cggccaaagggtt atctgcaagc 1980  
acttcgagca tatcaaactt caccaccagg actcttcaac atgatgttgc acaagattct 2040  
gaccagctt atagcagtgg gatgtttcac tgggtggaaac caacccctttt ggacaagggtt 2100  
actctgaaac gaactggcaat gtcggaaat aagtttccggaa accatattgtt agcatgttgc 2160  
tttggagatg cccactcagc cccggatgggg cttcgaaact ttgtatgttgc cttgagagcc 2220  
agcaactata ccaggaagga gctgaaggac atagtttca ttgggtctctt ggactatcta 2280  
cagagagaat ggcgatttttcccgatata acattcttgc tggatgttgc 2340

ctttatctcg gagacacctca	tgcgccaa	ataga	gcaat	gtccatgt	tgctgtctt	2400
tcccccccac cccagccatc	aagcaaccag	actttggtag	acacaga	ac	catcatggca	2460
accctcacca tcggatcctt	gcaaattgac	tccttccttq	acc	ccgtcacc	ctcagtgt	2520
gaggagactc caggttacac	aaatggacat	aatgagaaat	caaact	gccc	aaaagtcct	2580
atccttactg aactgaaaaa	tccttccaac	attcacttta	ttgaacagct	tttgtgact	2640	
gaagggtccc tccaagaaac	aaatctgcat	ctcagcaactg	ccttttctac	gggcactgt	2700	
ttttccagca gcttcttgg	ttctctgt	gccacggcct	tctacaattt	tcatgtcct	2760	
gaattgttc agatgttgt	gacaggagga	gtaagtttctc	agctggaa	aca	acatttagat	2820
aaggataaaag tctatgtgt	ggcagatagc	tgcacgtcgc	tcttgtctgg	aagaaaaccgg	2880	
tgtaa	cttacacgaa	accattttat	cagacgtt	aaac	tc	2940
acctttggac aactgttctg	tggctcatta	gatctttt	gaatcctgt	tgttgctt	3000	
taccgaataa ttgatgaaga	ggagctcaac	ccagaaaaca	aaagg	ttt	gtatccccgg	3060
ccagccaatg agttcaag	gctgccttca	gatctt	gtgt	tttgc	ccat	3120
actgctgtt ataaaaggaa	tgaagagt	tcattgc	aaa	agtcatat	ga	3180
aaagcatcac agacaacaga	ggacacattc	agacaca	aaat	tgtcctccca	cccat	3240
cagttactga gacattgtat	tcaccagtct	attcttacca	gccgaga	act	ccctct	3300
ctttcctaa qcaaata	agg					3319

<210> 18  
<211> 1081  
<212> PRT  
<213> *Homo sapiens*

<220>  
<223> human hSlo3-2 (hSlo3-2)

<400> 18  
 Met Phe Gln Thr Lys Leu Arg Asn Glu Thr Trp Glu Asp Leu Pro Lys  
 1 5 10 15  
 Met Ser Cys Thr Thr Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Phe  
 20 25 30  
 Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Ile Phe Arg Leu Ile  
 35 40 45  
 Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile  
 50 55 60  
 Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser  
 65 70 75 80  
 Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser  
 85 90 95  
 Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu  
 100 105 110  
 Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val  
 115 120 125  
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val  
 130 135 140  
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala  
 145 150 155 160  
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile  
 165 170 175

Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp  
 180 185 190  
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln  
 195 200 205  
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe  
 210 215 220  
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly  
 225 230 235 240  
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg  
 245 250 255  
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala  
 260 265 270  
 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu  
 275 280 285  
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe  
 290 295 300  
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ala Asn Lys Arg Lys  
 305 310 315 320  
 Tyr Thr Ser Ser Tyr Glu Ala Leu Lys Gly Lys Lys Phe Ile Val Val  
 325 330 335  
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe  
 340 345 350  
 Leu Arg Asp Lys Ser Gly Glu Ile Asn Thr Glu Ile Val Phe Leu Gly  
 355 360 365  
 Glu Thr Pro Pro Ser Leu Glu Leu Glu Thr Ile Phe Lys Cys Tyr Leu  
 370 375 380  
 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu  
 385 390 395 400  
 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn  
 405 410 415  
 Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg  
 420 425 430  
 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln  
 435 440 445  
 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp  
 450 455 460  
 Asn Trp Asp Thr Gly Asp Asn Ile Ile Cys Phe Ala Glu Leu Lys Leu  
 465 470 475 480  
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu  
 485 490 495

Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr  
 500 505 510  
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gin  
 515 520 525  
 Arg Leu Ser Asp Asp Phe Ala Gly Met Ser Phe Pro Glu Val Ala Arg  
 530 535 540  
 Gly Leu Ile Leu Asn Pro Pro Gln Val Arg Ile Arg Lys Asn Thr  
 545 550 555 560  
 Leu Gly Phe Phe Ile Ala Glu Thr Pro Lys Asp Val Arg Arg Ala Leu  
 565 570 575  
 Phe Tyr Cys Ser Val Cys His Asp Asp Val Phe Ile Pro Glu Leu Ile  
 580 585 590  
 Thr Asn Cys Gly Cys Lys Ser Arg Ser Arg Gln His Ile Thr Val Pro  
 595 600 605  
 Ser Val Lys Arg Met Lys Lys Cys Leu Lys Gly Ile Ser Ser Arg Ile  
 610 615 620  
 Ser Gly Gln Asp Ser Pro Pro Arg Val Ser Ala Ser Thr Ser Ser Ile  
 625 630 635 640  
 Ser Asn Phe Thr Thr Arg Thr Leu Gln His Asp Val Glu Gln Asp Ser  
 645 650 655  
 Asp Gln Leu Asp Ser Ser Gly Met Phe His Trp Cys Lys Pro Thr Ser  
 660 665 670  
 Leu Asp Lys Val Thr Leu Lys Arg Thr Gly Lys Ser Lys Tyr Lys Phe  
 675 680 685  
 Arg Asn His Ile Val Ala Cys Val Phe Gly Asp Ala His Ser Ala Pro  
 690 695 700  
 Met Gly Leu Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr  
 705 710 715 720  
 Arg Lys Glu Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Asp Tyr Leu  
 725 730 735  
 Gln Arg Glu Trp Arg Phe Leu Arg Asn Phe Pro Gln Ile Tyr Ile Leu  
 740 745 750  
 Pro Gly Cys Ala Leu Tyr Ser Gly Asp Leu His Ala Ala Asn Ile Glu  
 755 760 765  
 Gln Cys Ser Met Cys Ala Val Leu Ser Pro Pro Gln Pro Ser Ser  
 770 775 780  
 Asn Gln Thr Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Thr Ile  
 785 790 795 800  
 Gly Ser Leu Gln Ile Asp Ser Ser Asp Pro Ser Pro Ser Val Ser  
 805 810 815

Glu Glu Thr Pro Gly Tyr Thr Asn Gly His Asn Glu Lys Ser Asn Cys  
 820 825 830  
 Arg Lys Val Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His  
 835 840 845  
 Phe Ile Glu Gln Leu Gly Gly Leu Glu Gly Ser Leu Gln Glu Thr Asn  
 850 855 860  
 Leu His Leu Ser Thr Ala Phe Ser Thr Gly Thr Val Phe Ser Ser Ser  
 865 870 875 880  
 Phe Leu Asp Ser Leu Leu Ala Thr Ala Phe Tyr Asn Tyr His Val Leu  
 885 890 895  
 Glu Leu Leu Gln Met Leu Val Thr Gly Gly Val Ser Ser Gln Leu Glu  
 900 905 910  
 Gln His Leu Asp Lys Asp Lys Val Tyr Gly Val Ala Asp Ser Cys Thr  
 915 920 925  
 Ser Leu Leu Ser Gly Arg Asn Arg Cys Lys Leu Gly Leu Leu Ser Leu  
 930 935 940  
 His Glu Thr Ile Leu Ser Asp Val Asn Pro Arg Asn Thr Phe Gly Gln  
 945 950 955 960  
 Leu Phe Cys Gly Ser Leu Asp Leu Phe Gly Ile Leu Cys Val Gly Leu  
 965 970 975  
 Tyr Arg Ile Ile Asp Glu Glu Leu Asn Pro Glu Asn Lys Arg Phe  
 980 985 990  
 Val Ile Thr Arg Pro Ala Asn Glu Phe Lys Leu Leu Pro Ser Asp Leu  
 995 1000 1005  
 Val Phe Cys Ala Ile Pro Phe Ser Thr Ala Cys Tyr Lys Arg Asn Glu  
 1010 1015 1020  
 Glu Phe Ser Leu Gln Lys Ser Tyr Glu Ile Val Asn Lys Ala Ser Gln  
 1025 1030 1035 1040  
 Thr Thr Glu Asp Thr Phe Arg His Lys Leu Ser Ser His Pro Leu Ile  
 1045 1050 1055  
 Gln Leu Leu Arg His Cys Ile His Gln Ser Ile Leu Thr Ser Arg Glu  
 1060 1065 1070  
 Leu Thr Pro Ser Leu Phe Leu Ser Lys  
 1075 1080

<210> 19  
 <211> 3247  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human Slo3-2 (hSlo3-2)

<400> 19

atgtttcaga ctaagctacg aaatgaaact tggaaagact tgccaaaaat gtcctgcaca 60  
actgagatcc aagcagcatt cattctctt tccttgcata ccttcttcag tgactcatc 120  
atccgttga tcctcaggct gatctggaga tctgtaaaa aatggcaaat catcaaggga 180  
acaggaatta tcttggaaact gttcacatca ggtaccatcg cttaggagcca tgaagaagc 240  
ctccacttcc agggacaatt tcgtgatcat atagaatgt tgcttcagc ccagacctt 300  
gtggggcaag tgitgggtat cttgtctt gtactaagca ttgggtcttataatctat 360  
ttcatcaatt ctgctgaccc ttttggaaagc tgttcatcat atgaagacaa aaccattcct 420  
attgatttgg ttttcaatgc tttcttagt ttcttatttg gattgagggt tatggcagct 480  
gatgacaaga tcaagttctg gctggagatg aattcaatcg tagacatctt taccatccc 540  
ccaaccttta ttcttatttta ttgaaagagc aattggctag gtttaagggtt cctaagagcc 600  
ttgcgcctgc tagaactccc tcaaattctg caaattctac gagccatcaa gaccagtaac 660  
tcagtgaagt tttccaaact gctgtcaata attctcagta cctggttcac agctgcggga 720  
ttcattcacc tggggaaaa ttctgggtat ccctggctca aaggtagaaa ttacacagaat 780  
atatcatatt ttgagtcata ttacctggc atggcaacaa cgtcaaccgt tggatttgg 840  
gatgtggtag ccaagacatc cttaggacgg accttcatac tgttcttcac actggggagt 900  
ttgatattat ttgcgaacta tatacctgaa atggggaaac tgtttcttaa caagagggaa 960  
tacaccagtt cmtatgaagc actcaaagga aagaagtttta ttgtggctcg tggaaacatc 1020  
actgtggaca gtgtgaccgc tttcctggg aatttctcc gcgacaagtc aggagagatc 1080  
aacactgaaa ttgtttccct gggagaaacc cttccttctt tggaacttga aaccatattt 1140  
aaatgctact tggcctacac aacgttcatt tctggatctg caatgaatcg ggaggatctg 1200  
aggcgagttt cggtgaaatc tgcagaggca tgcctgatc tagccaatcc tttgtgcagt 1260  
gattccatg ctgaagatatttcaacatt atgagggtgc tctctatcaa gaactatgat 1320  
tctaccacca gaatcatcat acagatactg caatcccata acaaggtttta tctgccaag 1380  
attcccagct ggaactggga caccggagac aacatcatct ttgttgcata attaaaactt 1440  
ggatttatcg cccaaaggctg tttgggtccca ggcttgcata 1500  
gtggagcaaa aaaaaaggat tatgcctaaa cagacctggaa agaaacactt cttgaatagc 1560  
atgaaaaaca aaattctgac ccaacgtctc tctgtatgact ttgctggat gagcttctt 1620  
gaagttgccc gtggctgtat actaaatcca cttccacaag tgaggatacg taagaacaca 1680  
ttagggttct ttattgtca aactccaaag gacgtcgaaa gaggctgtt ttactgttca 1740  
gtctgtcatg atgatgtgtt cattcctgatc ctaattacaa actgtggctg caaaagcaga 1800  
agccggcagc acatcacatg gccatcggtt aagagaatgaa aaaaatgtct gaagggaaatc 1860  
tcctctcgta tatcaaggca ggattctccg ccaagggtat ctgcaagcac ttgcagcata 1920  
tcaaacttca ccaccaggac tcttcaacat gatgtagaac aagattctga ccagcttgcata 1980  
agcagtggga tggttcaactg gtgcaaaacc accctttgg acaagggtac tctgaaacaga 2040  
actggcaagt caaagataaa gtttggaaac cataattgtatc catgtgtatt tggagatgcc 2100  
cactcagccc cgatggggct tcggaactt gtaatgcctt tgagagccag caactataacc 2160  
aggaaggagc tgaaggacat agtgttcatc gggctctgg actatctaca gagagaatgg 2220  
cgatttctcc ggaattttcc ccagatatac attctgcctt gatgtgcact ttattctgg 2280  
gacctccatg cggccaaacat agagcaatgc tccatgtgtt ctgttgcacccccaccc 2340  
cagccatcaa gcaaccagac tttggtagac acagaagcca tcatggcaac cctcaccatc 2400  
ggatccttgc aaattgactc ctctctgtac ccgtcaccct cagtgtcaga ggagactcca 2460  
ggttacacaa atggacataa tgagaaatca aactgccaa aagtccctat cttactgaa 2520  
ctgaaaaatc ttccaacat tcacttattt gaacagctt gttgactgga agggccctc 2580  
caagaaacaa atctgcatac cagcactgccc tttctacgg gcactgtttt ttccagcagc 2640  
ttcttggatt ctctgtggc cacggccctt tacaattatc atgtcctggaa attgttgcata 2700  
atgctgggtga caggaggat aagttctcag ctgaaacaac atttagataa gataaaatgc 2760  
tatgggtgttgg cagatagctg cacgtcgctc ttgttgcataa gaaaccgggtt taagctgggg 2820  
cttctgtcc tacacgaaac cattttatca gacgttatac caagaaacac ctttggacaa 2880  
ctgttctgtt gtcatttgc tctttttggaa atcctgtgtt ttggcttata cccgataatt 2940  
gatgaagagg agctcaaccc agaaaacaaa aggtttgtga tcacccggcc agccaatgag 3000  
ttcaagctgc tgccttcaga tcttgggttt tggccatac cttcagcac tgcttgcata 3060  
aaaaggaatg aagagttctc attgcataaag tcatatgaaa ttgtaaataa agcatcacag 3120  
acaacagagg acacattcag acacaaatttgc tcctcccacc cattgattca gttactgaga 3180  
cattgttattc accagtctat ttttaccacg cggaaactaa cttccctctt tttcctaagc 3240  
aaatagt 3247

<210> 20  
 <211> 1134  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse Slo3 (mSlo3)

<400> 20  
 Met Ser Gln Thr Leu Leu Asp Ser Leu Asn Gln Lys Glu Leu Thr Glu  
 1 5 10 15

Thr Ser Cys Thr Ile Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Leu  
 20 25 30

Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala  
 35 40 45

Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu  
 50 55 60

Leu Glu Leu Phe Ser Ser Arg Arg Ile Glu Ala Asn Pro Leu Arg Lys  
 65 70 75 80

Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser  
 85 90 95

Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu  
 100 105 110

Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val  
 115 120 125

Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser  
 130 135 140

Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala  
 145 150 155 160

Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile  
 165 170 175

Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp  
 180 185 190

Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys  
 195 200 205

Ile Leu Gln Ile Leu Gln Val Ile Lys Thr Ser Asn Ser Val Lys Leu  
 210 215 220

Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly  
 225 230 235 240

Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg  
 245 250 255

Asn Ser Gln Thr Met Ser Tyr Phe Glu Ser Ile Tyr Leu Val Thr Ala  
 260 265 270

Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu  
 275 280 285  
 Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe  
 290 295 300  
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys  
 305 310 315 320  
 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val  
 325 330 335  
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe  
 340 345 350  
 Leu His Trp Lys Ser Gly Glu Ile Asn Ile Glu Ile Val Phe Leu Gly  
 355 360 365  
 Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr  
 370 375 380  
 Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu  
 385 390 395 400  
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn  
 405 410 415  
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg  
 420 425 430  
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln  
 435 440 445  
 Ile Leu Gln Ser Gln Asn Lys Val Phe Leu Ser Lys Ile Pro Asn Trp  
 450 455 460  
 Asp Trp Ser Ala Gly Asp Asn Ile Leu Cys Phe Ala Glu Leu Lys Leu  
 465 470 475 480  
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu  
 485 490 495  
 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro  
 500 505 510  
 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln  
 515 520 525  
 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg  
 530 535 540  
 Leu Cys Phe Val Lys Leu Asn Leu Met Leu Ile Ala Ile Gln His Lys  
 545 550 555 560  
 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln  
 565 570 575  
 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser  
 580 585 590

Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp  
 595 600 605  
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser  
 610 615 620  
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu  
 625 630 635 640  
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu  
 645 650 655  
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr  
 660 665 670  
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu  
 675 680 685  
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys  
 690 695 700  
 Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His  
 705 710 715 720  
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu  
 725 730 735  
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu  
 740 745 750  
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu  
 755 760 765  
 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser  
 770 775 780  
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser  
 785 790 795 800  
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile  
 805 810 815  
 Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu  
 820 825 830  
 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro  
 835 840 845  
 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile  
 850 855 860  
 Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu  
 865 870 875 880  
 Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu  
 885 890 895  
 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp  
 900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu  
 915 920 925  
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu  
 930 935 940  
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys  
 945 950 955 960  
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr  
 965 970 975  
 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys  
 980 985 990  
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met  
 995 1000 1005  
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr  
 1010 1015 1020  
 Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys  
 1025 1030 1035 1040  
 Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe  
 1045 1050 1055  
 Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro  
 1060 1065 1070  
 Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile  
 1075 1080 1085  
 Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr  
 1090 1095 1100  
 Pro Glu Ser Ile Leu Trp Thr Arg Gln Leu Phe Cys Gly Ser Leu Asp  
 1105 1110 1115 1120  
 Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met Ile Asp  
 1125 1130

<210> 21  
 <211> 1236  
 <212> PRT  
 <213> Mus musculus  
  
 <220>  
 <223> mouse Slol (mSlol)

<400> 21  
 Met Asp Ala Leu Ile Ile Pro Val Thr Met Glu Val Pro Cys Asp Ser  
 1 5 10 15  
 Arg Gly Gln Arg Met Trp Trp Ala Phe Leu Ala Ser Ser Met Val Thr  
 20 25 30  
 Phe Phe Gly Gly Leu Phe Ile Ile Leu Leu Trp Arg Thr Leu Lys Tyr  
 35 40 45

Leu Trp Thr Val Cys Cys His Cys Gly Gly Lys Thr Lys Glu Ala Gln  
       50                  55                  60

Lys Ile Asn Asn Gly Ser Ser Gln Ala Asp Gly Thr Leu Lys Pro Val  
       65                  70                  75                  80

Asp Glu Lys Glu Glu Val Val Ala Ala Glu Val Gly Trp Met Thr Ser  
       85                  90                  95

Val Lys Asp Trp Ala Gly Val Met Ile Ser Ala Gln Thr Leu Thr Gly  
       100                105                110

Arg Val Leu Val Val Leu Val Phe Ala Leu Ser Ile Gly Ala Leu Val  
       115                120                125

Ile Tyr Phe Ile Asp Ser Ser Asn Pro Ile Glu Ser Cys Gln Asn Phe  
       130                135                140

Tyr Lys Asp Phe Thr Leu Gln Ile Asp Met Ala Phe Asn Val Phe Phe  
       145                150                155                160

Leu Leu Tyr Phe Gly Leu Arg Phe Ile Ala Ala Asn Asp Lys Leu Trp  
       165                170                175

Phe Trp Leu Glu Val Asn Ser Val Val Asp Phe Phe Thr Val Pro Pro  
       180                185                190

Val Phe Val Ser Val Tyr Leu Asn Arg Ser Trp Leu Gly Leu Arg Phe  
       195                200                205

Leu Arg Ala Leu Arg Leu Ile Gln Phe Ser Glu Ile Leu Gln Phe Leu  
       210                215                220

Asn Ile Leu Lys Thr Ser Asn Ser Ile Lys Leu Val Asn Leu Leu Ser  
       225                230                235                240

Ile Phe Ile Ser Thr Trp Leu Thr Ala Ala Gly Phe Ile His Leu Val  
       245                250                255

Glu Asn Ser Gly Asp Pro Trp Glu Asn Phe Gln Asn Asn Gln Ala Leu  
       260                265                270

Thr Tyr Trp Glu Cys Val Tyr Leu Leu Met Val Thr Met Ser Thr Val  
       275                280                285

Gly Tyr Gly Asp Val Tyr Ala Lys Thr Thr Leu Gly Arg Leu Phe Met  
       290                295                300

Val Phe Phe Ile Leu Gly Gly Leu Ala Met Phe Ala Ser Tyr Val Pro  
       305                310                315                320

Glu Ile Ile Glu Leu Ile Gly Asn Arg Lys Lys Tyr Gly Gly Ser Tyr  
       325                330                335

Ser Ala Val Ser Gly Arg Lys His Ile Val Val Cys Gly His Ile Thr  
       340                345                350

Leu Glu Ser Val Ser Asn Phe Leu Lys Asp Phe Leu His Lys Asp Arg  
       355                360                365

Asp Asp Val Asn Val Glu Ile Val Phe Leu His Asn Ile Ser Pro Asn  
 370 375 380  
 Leu Glu Leu Glu Ala Leu Phe Lys Arg His Phe Thr Gln Val Glu Phe  
 385 390 395 400  
 Tyr Gin Gly Ser Val Leu Asn Pro His Asp Leu Ala Arg Val Lys Ile  
 405 410 415  
 Glu Ser Ala Asp Ala Cys Leu Ile Leu Ala Asn Lys Tyr Cys Ala Asp  
 420 425 430  
 Pro Asp Ala Glu Asp Ala Ser Asn Ile Met Arg Val Ile Ser Ile Lys  
 435 440 445  
 Asn Tyr His Pro Lys Ile Arg Ile Ile Thr Gln Met Leu Gln Tyr His  
 450 455 460  
 Asn Lys Ala His Leu Leu Asn Ile Pro Ser Trp Asn Trp Lys Glu Gly  
 465 470 475 480  
 Asp Asp Ala Ile Cys Leu Ala Glu Leu Lys Leu Gly Phe Ile Ala Gln  
 485 490 495  
 Ser Cys Leu Ala Gln Gly Leu Ser Thr Met Leu Ala Asn Leu Phe Ser  
 500 505 510  
 Met Arg Ser Phe Ile Lys Ile Glu Glu Asp Thr Trp Gln Lys Tyr Tyr  
 515 520 525  
 Leu Glu Gly Val Ser Asn Glu Met Tyr Thr Glu Tyr Leu Ser Ser Ala  
 530 535 540  
 Phe Val Gly Leu Ser Phe Pro Thr Val Cys Glu Leu Cys Phe Val Lys  
 545 550 555 560  
 Leu Lys Leu Leu Met Ile Ala Ile Glu Tyr Lys Ser Ala Asn Arg Glu  
 565 570 575  
 Ser Arg Ile Leu Ile Asn Pro Gly Asn His Leu Lys Ile Gln Glu Gly  
 580 585 590  
 Thr Leu Gly Phe Phe Ile Ala Ser Asp Ala Lys Glu Val Lys Arg Ala  
 595 600 605  
 Phe Phe Tyr Cys Lys Ala Cys His Asp Asp Val Thr Asp Pro Lys Arg  
 610 615 620  
 Ile Lys Lys Cys Gly Cys Arg Arg Leu Ile Tyr Phe Glu Asp Glu Gln  
 625 630 635 640  
 Pro Pro Thr Leu Ser Pro Lys Lys Gln Arg Asn Gly Gly Met Arg  
 645 650 655  
 Asn Ser Pro Asn Thr Ser Pro Lys Leu Met Arg His Asp Pro Leu Leu  
 660 665 670  
 Ile Pro Gly Asn Asp Gln Ile Asp Asn Met Asp Ser Asn Val Lys Lys  
 675 680 685

Tyr Asp Ser Thr Gly Met Phe His Trp Cys Ala Pro Lys Glu Ile Glu  
 690 695 700  
 Lys Val Ile Leu Thr Arg Ser Glu Ala Ala Met Thr Val Leu Ser Gly  
 705 710 715 720  
 His Val Val Val Cys Ile Phe Gly Asp Val Ser Ser Ala Leu Ile Gly  
 725 730 735  
 Leu Arg Asn Leu Val Met Pro Leu Arg Ala Ser Asn Phe His Tyr His  
 740 745 750  
 Glu Leu Lys His Ile Val Phe Val Gly Ser Ile Glu Tyr Leu Lys Arg  
 755 760 765  
 Glu Trp Glu Thr Leu His Asn Phe Pro Lys Val Ser Ile Leu Pro Gly  
 770 775 780  
 Thr Pro Leu Ser Arg Ala Asp Leu Arg Ala Val Asn Ile Asn Leu Cys  
 785 790 795 800  
 Asp Met Cys Val Ile Leu Ser Ala Asn Gln Asn Asn Ile Asp Asp Thr  
 805 810 815  
 Ser Leu Gln Asp Lys Glu Cys Ile Leu Ala Ser Leu Asn Ile Lys Ser  
 820 825 830  
 Met Gln Phe Asp Asp Ser Ile Gly Val Leu Gln Ala Asn Ser Gln Gly  
 835 840 845  
 Phe Thr Pro Pro Gly Met Asp Arg Ser Ser Pro Asp Asn Ser Pro Val  
 850 855 860  
 His Gly Met Leu Arg Gln Pro Ser Ile Thr Thr Gly Val Asn Ile Pro  
 865 870 875 880  
 Ile Ile Thr Glu Leu Val Asn Asp Thr Asn Val Gln Phe Leu Asp Gln  
 885 890 895  
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe  
 900 905 910  
 Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser  
 915 920 925  
 Ala Thr Tyr Phe Asn Asp Asn Ile Leu Thr Leu Ile Arg Thr Leu Val  
 930 935 940  
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Ala Leu Ile Ala Glu Glu Asn  
 945 950 955 960  
 Ala Leu Arg Gly Gly Tyr Ser Thr Pro Gln Thr Leu Ala Asn Arg Asp  
 965 970 975  
 Arg Cys Arg Val Ala Gln Leu Ala Leu Leu Asp Gly Pro Phe Ala Asp  
 980 985 990  
 Leu Gly Asp Gly Gly Cys Tyr Gly Asp Leu Phe Cys Lys Ala Leu Lys  
 995 1000 1005

Thr Tyr Asn Met Leu Cys Phe Gly Ile Tyr Arg Leu Arg Asp Ala His  
 1010 1015 1020  
 Leu Ser Thr Pro Ser Gln Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro  
 1025 1030 1035 1040  
 Pro Tyr Glu Phe Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met  
 1045 1050 1055  
 Gln Phe Asp His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser  
 1060 1065 1070  
 Ser His Ser Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser  
 1075 1080 1085  
 Ile Pro Ser Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser  
 1090 1095 1100  
 Arg Asp Lys Gln Asn Ala Thr Arg Met Thr Arg Met Gly Gln Ala Glu  
 1105 1110 1115 1120  
 Lys Lys Trp Phe Thr Asp Glu Pro Asp Asn Ala Tyr Pro Arg Asn Ile  
 1125 1130 1135  
 Gln Ile Lys Pro Met Ser Thr His Met Ala Asn Gln Ile Asn Gln Tyr  
 1140 1145 1150  
 Lys Ser Thr Ser Ser Leu Ile Pro Pro Ile Arg Glu Val Glu Asp Glu  
 1155 1160 1165  
 Cys Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp  
 1170 1175 1180  
 His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser  
 1185 1190 1195 1200  
 Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro Ser  
 1205 1210 1215  
 Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser Arg Asp Lys  
 1220 1225 1230  
 Gln Asn Ala Thr  
 1235

<210> 22  
 <211> 1262  
 <212> PRT  
 <213> Drosophila sp.

<220>  
 <223> Drosophila Slo1 (dSlo1)

<400> 22  
 Met Ala Ser Gly Leu Ile Asp Thr Asn Phe Ser Ser Thr Leu Ala Asn  
 1 5 10 15

Gly Met Ser Gly Cys Asp Gln Ser Thr Val Glu Pro Leu Ala Asp Asp  
 20 25 30

Pro Thr Asp Ser Pro Phe Asp Ala Asp Asp Cys Leu Lys Val Arg Lys  
 35 40 45  
 Tyr Trp Cys Phe Leu Leu Ser Ser Ile Phe Thr Phe Leu Ala Gly Leu  
 50 55 60  
 Leu Val Val Leu Leu Trp Arg Ala Phe Ala Phe Val Ser Cys Arg Lys  
 65 70 75 80  
 Glu Pro Asp Leu Gly Pro Asn Asp Pro Lys Gln Lys Glu Gln Lys Ala  
 85 90 95  
 Ser Arg Asn Lys Gln Glu Phe Glu Gly Thr Phe Met Thr Glu Ala Lys  
 100 105 110  
 Asp Trp Ala Gly Glu Leu Ile Ser Gly Gln Thr Thr Thr Gly Arg Ile  
 115 120 125  
 Leu Val Val Leu Val Phe Ile Leu Ser Ile Ala Ser Leu Ile Ile Tyr  
 130 135 140  
 Phe Val Asp Ala Ser Ser Glu Glu Val Glu Arg Cys Gln Lys Trp Ser  
 145 150 155 160  
 Asn Asn Ile Thr Gln Gln Ile Asp Leu Ala Phe Asn Ile Phe Phe Met  
 165 170 175  
 Val Tyr Phe Phe Ile Arg Phe Ile Ala Ala Ser Asp Lys Leu Trp Phe  
 180 185 190  
 Met Leu Glu Met Tyr Ser Phe Val Asp Tyr Phe Thr Ile Pro Pro Ser  
 195 200 205  
 Phe Val Ser Ile Tyr Leu Asp Arg Thr Trp Ile Gly Leu Arg Phe Leu  
 210 215 220  
 Arg Ala Leu Arg Leu Met Thr Val Pro Asp Ile Leu Gln Tyr Leu Asn  
 225 230 235 240  
 Val Leu Lys Thr Ser Ser Ile Arg Leu Ala Gln Leu Val Ser Ile  
 245 250 255  
 Phe Ile Ser Val Trp Leu Thr Ala Ala Gly Ile Ile His Leu Leu Glu  
 260 265 270  
 Asn Ser Gly Asp Pro Leu Asp Phe Asn Asn Ala His Arg Leu Ser Tyr  
 275 280 285  
 Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr  
 290 295 300  
 Gly Asp Val Tyr Cys Glu Thr Val Leu Gly Arg Thr Phe Leu Val Phe  
 305 310 315 320  
 Phe Leu Leu Val Gly Leu Ala Val Phe Ala Ser Trp Ile Pro Glu Ile  
 325 330 335  
 Thr Glu Leu Ala Ala Gln Arg Ser Lys Tyr Gly Gly Thr Tyr Ser Lys  
 340 345 350

Asp Pro Arg Lys Arg His Ile Val Val Cys Gly His Ile Thr Tyr Glu  
     355                         360                         365  
  
 Ser Val Ser His Phe Leu Lys Asp Phe Leu His Glu Asp Arg Glu Asp  
     370                         375                         380  
  
 Val Asp Val Glu Val Val Phe Leu His Arg Lys Pro Pro Asp Leu Glu  
     385                         390                         395                         400  
  
 Leu Glu Gly Leu Phe Lys Arg His Phe Thr Thr Val Glu Phe Phe Gln  
     405                         410                         415  
  
 Gly Thr Ile Met Asn Pro Ile Asp Leu Gln Arg Val Lys Val His Glu  
     420                         425                         430  
  
 Ala Asp Ala Cys Leu Val Leu Ala Asn Lys Tyr Cys Gln Asp Pro Asp  
     435                         440                         445  
  
 Ala Glu Asp Ala Ala Asn Ile Met Arg Val Ile Ser Ile Lys Asn Tyr  
     450                         455                         460  
  
 Ser Asp Asp Ile Arg Val Ile Ile Gln Leu Met Gln Tyr His Asn Lys  
     465                         470                         475                         480  
  
 Ala Tyr Leu Leu Asn Ile Pro Ser Trp Asp Trp Lys Gln Gly Asp Asp  
     485                         490                         495  
  
 Val Ile Cys Leu Ala Glu Leu Lys Leu Gly Phe Ile Ala Gln Ser Cys  
     500                         505                         510  
  
 Leu Ala Pro Gly Phe Ser Thr Met Met Ala Asn Leu Phe Ala Met Arg  
     515                         520                         525  
  
 Ser Phe Lys Thr Ser Pro Asp Met Gln Ser Trp Thr Asn Asp Tyr Leu  
     530                         535                         540  
  
 Arg Gly Thr Gly Met Glu Met Tyr Thr Glu Thr Leu Ser Pro Thr Phe  
     545                         550                         555                         560  
  
 Ile Gly Ile Pro Phe Ala Gln Ala Thr Glu Leu Cys Phe Ser Lys Leu  
     565                         570                         575  
  
 Lys Leu Leu Leu Ala Ile Glu Ile Lys Gly Ala Glu Glu Gly Ala  
     580                         585                         590  
  
 Asp Ser Lys Ile Ser Ile Asn Pro Arg Gly Ala Lys Ile Gln Ala Asn  
     595                         600                         605  
  
 Thr Gln Gly Phe Phe Ile Ala Gln Ser Ala Asp Glu Val Lys Arg Ala  
     610                         615                         620  
  
 Trp Phe Tyr Cys Lys Ala Cys His Glu Asp Ile Lys Asp Glu Thr Leu  
     625                         630                         635                         640  
  
 Ile Lys Lys Cys Lys Cys Lys Asn Leu Thr Val Gln Pro Arg Ser Lys  
     645                         650                         655  
  
 Phe Asp Asp Leu Gly Asp Ile Thr Arg Asp Arg Glu Asp Thr Asn Leu  
     660                         665                         670

Leu Asn Arg Asn Val Arg Arg Pro Asn Gly Thr Gly Asn Gly Thr Gly  
 675 680 685  
 Gly Met His His Met Asn Ser Thr Arg Ala Ala Ala Ala Ala Ala  
 690 695 700  
 Ala Ala Gly Lys Gln Val Asn Lys Val Lys Pro Thr Val Asn Val Ser  
 705 710 715 720  
 Arg Gln Val Glu Gly Gln Val Ile Ser Pro Ser Gln Tyr Asn Arg Pro  
 725 730 735  
 Thr Ser Arg Ser Ser Gly Thr Gly Thr Gln Asn Gln Asn Gly Gly Val  
 740 745 750  
 Ser Leu Pro Ala Gly Ile Ala Asp Asp Gln Ser Lys Asp Phe Asp Phe  
 755 760 765  
 Glu Lys Thr Glu Met Lys Tyr Asp Ser Thr Gly Met Phe His Trp Ser  
 770 775 780  
 Pro Ala Lys Ser Leu Gln Asp Cys Ile Leu Asp Arg Asn Gln Ala Ala  
 785 790 795 800  
 Met Thr Val Leu Asn Gly His Val Val Val Cys Leu Phe Ala Asp Pro  
 805 810 815  
 Asp Ser Pro Leu Ile Gly Leu Arg Asn Leu Val Met Pro Leu Arg Ala  
 820 825 830  
 Ser Asn Phe His Tyr His Glu Leu Lys His Val Val Ile Val Gly Ser  
 835 840 845  
 Val Asp Tyr Ile Arg Arg Glu Trp Lys Met Leu Gln Asn Leu Pro Lys  
 850 855 860  
 Ile Ser Val Leu Asn Gly Ser Pro Leu Ser Arg Ala Asp Leu Arg Ala  
 865 870 875 880  
 Val Asn Val Asn Leu Cys Asp Met Cys Cys Ile Leu Ser Ala Lys Val  
 885 890 895  
 Pro Ser Asn Asp Asp Pro Thr Leu Ala Asp Lys Glu Ala Ile Leu Ala  
 900 905 910  
 Ser Leu Asn Ile Lys Ala Met Thr Phe Asp Asp Thr Ile Gly Val Leu  
 915 920 925  
 Ser Gln Arg Gly Pro Glu Phe Asp Asn Leu Ser Ala Thr Ala Gly Ser  
 930 935 940  
 Pro Ile Val Leu Gln Arg Arg Gly Ser Val Tyr Gly Ala Asn Val Pro  
 945 950 955 960  
 Met Ile Thr Glu Leu Val Asn Asp Gly Asn Val Gln Phe Leu Asp Gln  
 965 970 975  
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe  
 980 985 990

Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser  
 995 1000 1005  
 Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile  
 1010 1015 1020  
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Leu Ala Glu Gly Ala  
 1025 1030 1035 1040  
 Gly Leu Arg Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp  
 1045 1050 1055  
 Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln  
 1060 1065 1070  
 Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys  
 1075 1080 1085  
 Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser  
 1090 1095 1100  
 Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro  
 1105 1110 1115 1120  
 Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln  
 1125 1130 1135  
 Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala  
 1140 1145 1150  
 Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly  
 1155 1160 1165  
 Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val  
 1170 1175 1180  
 Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys  
 1185 1190 1195 1200  
 Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met  
 1205 1210 1215  
 Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Cys Asp  
 1220 1225 1230  
 Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro Asp Asp Phe Ser  
 1235 1240 1245  
 Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln Phe Asp  
 1250 1255 1260

<210> 23  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:sense  
 oligonucleotide

<400> 23  
gtggatgata ccgacatgtt ggac

24

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:antisense  
oligonucleotide

<400> 24  
gagaccacct ctctcccgta tcgt

24

<210> 25  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:mSlo3 (S4 to  
S5) sense primer

<400> 25  
ctcgaactcc ctaaaatctt acagat

26

<210> 26  
<211> 28-  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:mSlo3 (S4 to  
S5) antisense primer

<400> 26  
ttccgttgag ccaggggtca ccagaatt

28

<210> 27  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:mSlo3 (S8 to  
S9) sense primer

<400> 27  
tctgctttgt gaagctaaat ct

22

<210> 28  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSl03 (S8 to  
S9) antisense primer

<400> 28  
tttcaaagcc tcttttagcgg taa

23

<210> 29  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSl03 (S9 to  
S10) sense primer

<400> 29  
ttatgcctgg atctgcactc tacatg

26

<210> 30  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:mSl03 (S9 to  
S10) antisense primer

<400> 30  
atagttccg tctactaccg aaa

23

<210> 31  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:control human  
beta-actin sense primer

<400> 31  
gatgatatcg ccgcgcgtcg cgtcgac

27

<210> 32  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:control human  
beta-actin antisense primer

<400> 32  
tcggtccagg tctgcgtcct accgtac

27

<210> 33  
<211> 28  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:northern blot  
sense primer

<400> 33  
cgaaaaacgtc atgtacaatc gaaatcca

28

<210> 34  
<211> 28  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:northern blot  
antisense primer

<400> 34  
ttccgttgag ccaggggtca ccagaatt

28

<210> 35  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:human testis  
cDNA library primer

<400> 35  
ggcagcgctc attcttcct cctt

24

<210> 36  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:human testis  
cDNA library primer

<400> 36  
tgcccaaaac ctcaacccaa aata

24

<210> 37  
<211> 4  
<212> PRT  
<213> Mus musculus  
  
<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo3 Region A peptide starting at amino acid 792

<400> 37  
Ile Ala Val Asn  
1

<210> 38  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo3 Region A peptide ending at amino acid 870

<400> 38  
Leu Thr Glu Leu  
1

<210> 39  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo1 Region A peptide starting at amino acid 793

<400> 39  
Arg Ala Val Asn  
1

<210> 40  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo1 Region A peptide ending at amino acid 885

<400> 40  
Ile Thr Glu Leu  
1

<210> 41  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo3 Region B peptide starting at amino acid 871

<400> 41  
Lys Asn Pro Ser  
1

<210> 42  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo3 Region B peptide ending at amino acid 906

<400> 42  
Gly Ala Val Phe  
1

<210> 43  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo1 Region B peptide starting at amino acid 886

<400> 43  
Val Asn Asp Thr  
1

<210> 44  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(4)  
<223> mSlo1 Region B peptide ending at amino acid 918

<400> 44  
Gly Thr Ala Phe  
1

<210> 45  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:hybrid of mSlo1 and mSlo3 sequences at C-terminal end of chimera Region B fragment

<400> 45  
Gly Ala Ala Phe  
1

<210> 46  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo3 Region C peptide starting at amino acid 899

<400> 46  
Ser Thr Ser Phe  
1

<210> 47  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo3 Region C peptide ending at amino acid 941

<400> 47  
Ser Glu Met Glu  
1

<210> 48  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlol Region C peptide starting at amino acid 909

<400> 48  
Thr Gln Pro Phe  
1

<210> 49  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlol Region C peptide ending at amino acid 963

<400> 49  
Pro Glu Leu Glu  
1

<210> 50  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo3 Region D peptide starting at amino acid 939

<400> 50  
Glu Met Glu His  
1

<210> 51  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo3 Region D peptide ending at amino acid 1034

<400> 51  
His Leu Leu Pro  
1

<210> 52  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo1 Region D peptide starting at amino acid 951

<400> 52  
Glu Leu Glu Ala  
1

<210> 53  
<211> 4  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(4)  
<223> mSlo1 Region D peptide ending at amino acid 1048

<400> 53  
Glu Leu Val Pro  
1